Fig. 1A

P6 AciI
2931 2905 2907 2909 2911
25bp 2904 2906 2908 2910

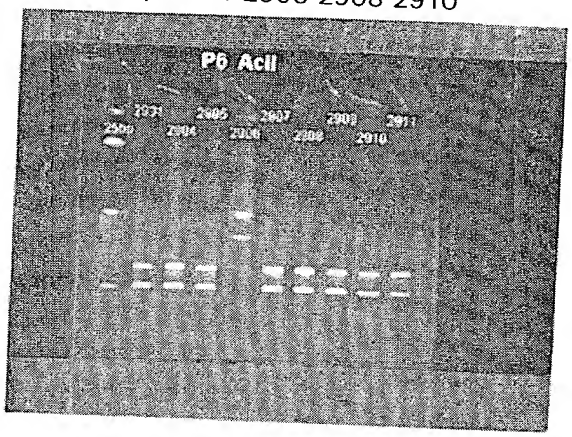

Fig. 1B

P6 AciI
2912 2926 2956 2969
25bp 2913 2931 2960 2975

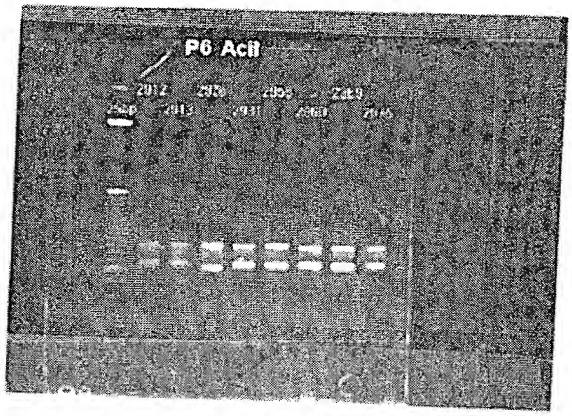

Fig. 1C

P6 AluI
2931 2905 2907 2909 2911
25bp 2904 2906 2908 2910

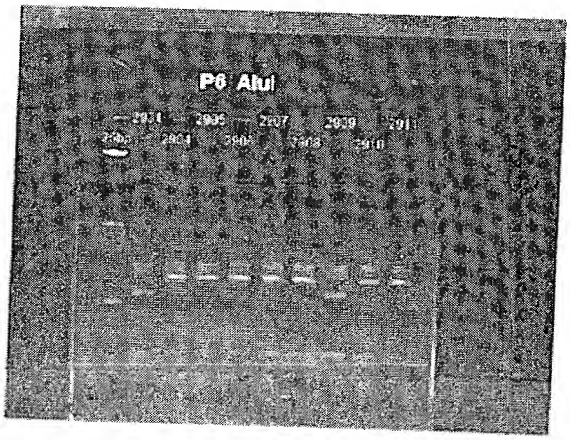

Fig. 1D

P6 AluI
2912 2926 2956 2969
25bp 2913 2931 2960 2975

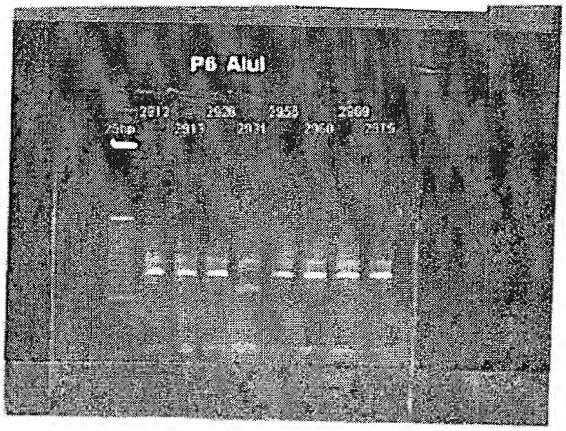

Fig. 1E

P6 Bbvl
2931 2905 2907 2909 2911
25bp 2904 2906 2908 2910

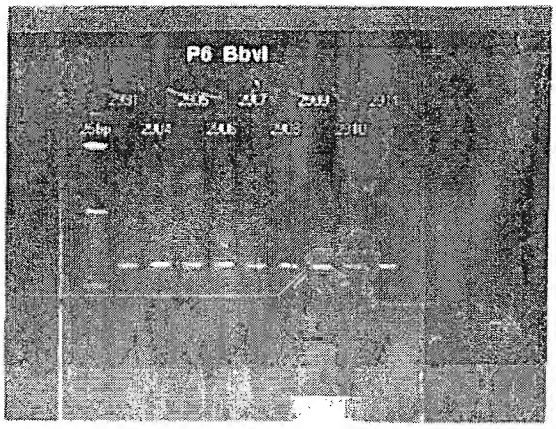

Fig. 1F

P6 Bbvl
2912 2926 2956 2969
25bp 2913 2931 2960 2975

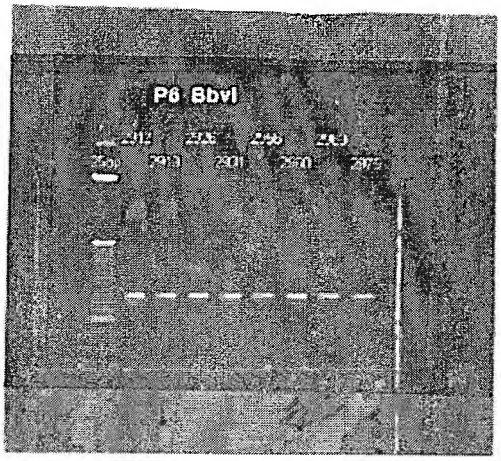

Fig. 1G

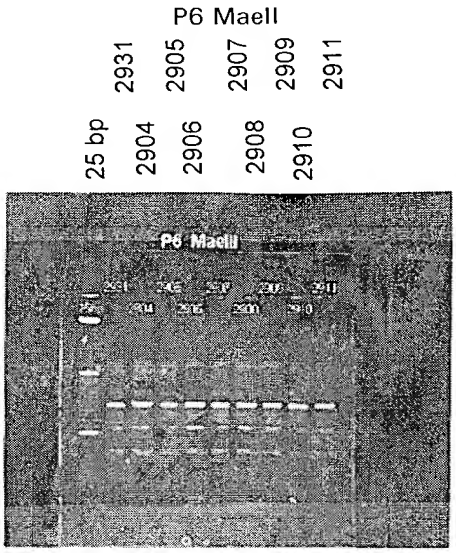

Fig. 1H

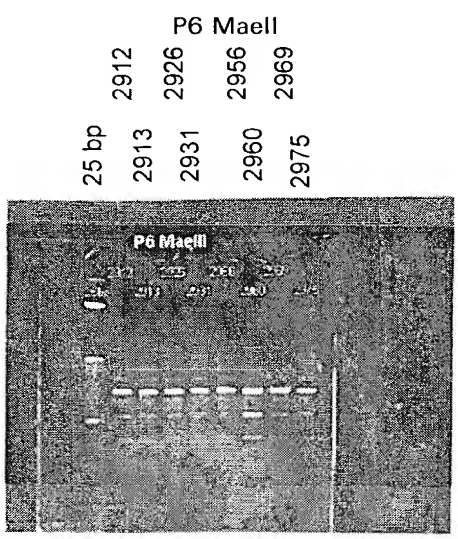

Fig. 1I

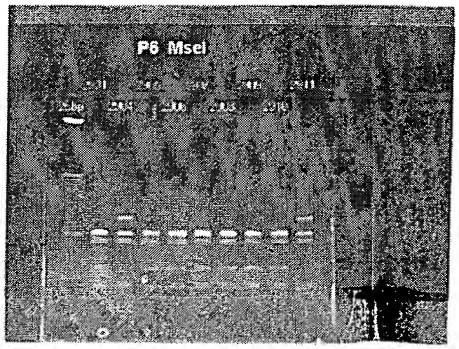

Fig. 1J

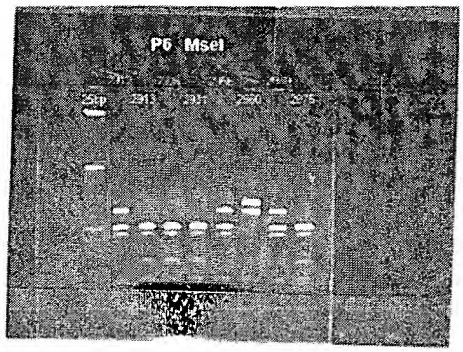

Fig. 1K

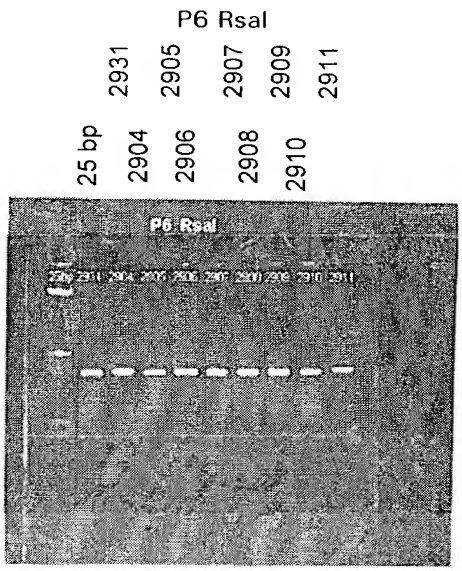

Fig. 1L

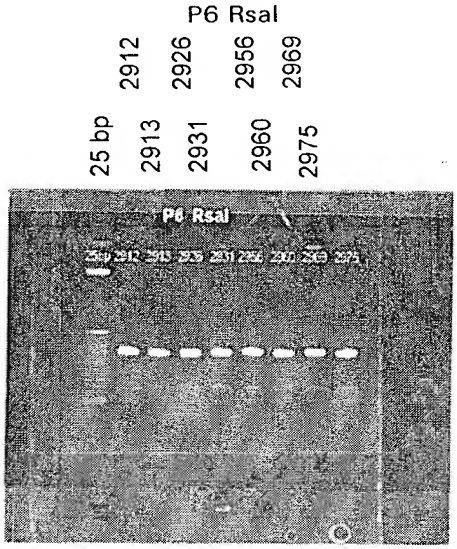

Fig. 2A

Identity to SeqID No:1 is indicated by a dot.

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                  *         20          *         40          *
Seqid1   :  ATGATGTTACATATTCAAATTGCCGCCGCTGCCGCCGCTTTATCGGTACT
:  50
Seqid3   :  ..................................................
:  50
Seqid5   :  ..................................................
:  50
Seqid7   :  ........................T.........................
:  50

                 60          *         80          *        100
Seqid1   :  AACTTTTATGACAGGCTGTGCCAATAAATCAACAAGTCAAGTTATGGTTG
: 100
Seqid3   :  ..................................................
: 100
Seqid5   :  ..................................................
: 100
Seqid7   :  ..................................................
: 100

                  *        120          *        140          *
Seqid1   :  CTCCTAATGCACCCACAGGTTACACTGGGGTTATCTATACTGGTGTTGCA
: 150
Seqid3   :  ..................................................
: 150
Seqid5   :  ..................................................
: 150
Seqid7   :  ..............G......G....C........C.............
: 150
```

Fig. 2B

```
                160         *       180         *       200
Seqid1  :  CCTTTGGTAGATAATGATGAGACCGTTAAGGCTCTGGCAAGCAAGCTACC
: 200
Seqid3  :  ....................................A.......C......
: 200
Seqid5  :  ......................TA.C...A..T.........C......
: 200
Seqid7  :  ........................C......T.........C......
: 200

                *       220         *       240         *
Seqid1  :  CAGTTTGGTTTATTTTGACTTTGATTCTGATGAGATTAAACCGCAAGCTG
: 250
Seqid3  :  ..................................................
: 250
Seqid5  :  ..................................................
: 250
Seqid7  :  ..................................................
: 250

                260         *       280         *       300
Seqid1  :  CTGCCATCTTAGACGAACAAGCACAATTTTTAACCACCAATCAAACAGCT
: 300
Seqid3  :  ..................................................
: 300
Seqid5  :  ..................................................
: 300
Seqid7  :  ..................................................
: 300
```

Fig. 2C

```
                  *       320         *       340         *
Seqid1  :  CGTGTTTTGGTTGCAGGTCATACCGATGAGCGTGGTAGTCGTGAGTATAA
: 350
Seqid3  :  ..................................................
: 350
Seqid5  :  ..................................................
: 350
Seqid7  :  ..................................................
: 350

                360         *       380         *       400
Seqid1  :  TATGTCACTGGGGGAACGCCGTGCGGTGGCGGTACGCAACTATTTGCTTG
: 400
Seqid3  :  ................T.................................
: 400
Seqid5  :  ..................................................
: 400
Seqid7  :  ..................................................A
: 400

                  *       420         *       440         *
Seqid1  :  GTAAAGGCATTAATCAAGCCAGCGTTGAGATTATCAGTTTTGGTGAAGAA
: 450
Seqid3  :  ..................................................
: 450
Seqid5  :  ..................................................
: 450
Seqid7  :  .........C........................................
: 450
```

Fig. 2D

```
                460         *       480         *       500
Seqid1  :  CGCCCTATCGCATTTGGCACAAATGAAGAAGCATGGTCACAAAATCGTCG
: 500
Seqid3  :  ..................................................
: 500
Seqid5  :  ..................................................
: 500
Seqid7  :  ..................................................
: 500


                  *
Seqid1 : TGCTGAACTGTCTTATTAA : 519
Seqid3 : ................... : 519
Seqid5 : ................... : 519
Seqid7 : ................... : 519
```

Fig. 3A

Identity to SeqID No:2 is indicated by a dot.

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                  *         20          *         40          *
Seqid2   :  MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVA
:  50
Seqid4   :  ..................................................
:  50
Seqid6   :  ..................................................
:  50
Seqid8   :  ..........................................A.......
:  50

                 60          *         80          *        100
Seqid2   :  PLVDNDETVKALASKLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTA
: 100
Seqid4   :  ..............T...................................
: 100
Seqid6   :  ........I.T...T...................................
: 100
Seqid8   :  ..............T...................................
: 100

                  *        120          *        140          *
Seqid2   :  RVLVAGHTDERGSREYNMSLGERRAVAVRNYLLGKGINQASVEIISFGEE
: 150
Seqid4   :  ..................................................
: 150
Seqid6   :  ..................................................
: 150
Seqid8   :  ..................................S...............
: 150
```

Fig. 3B

```
                  160         *
Seqid2 : RPIAFGTNEEAWSQNRRAELSY : 172
Seqid4 : ....................... : 172
Seqid6 : ....................... : 172
Seqid8 : ....................... : 172
```

Figure 4: Coomasie stained SDS-PAGE of BASB019 protein

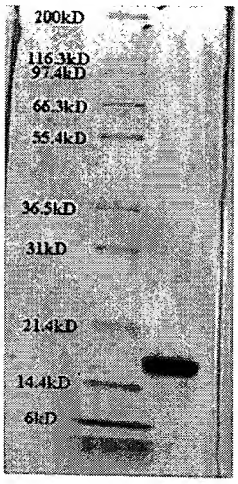

Figure 5: Western-blot with tetra-His antibody of BASB019 protein

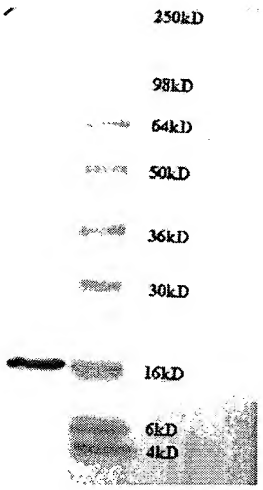

Figure 6: Western-blot of purified recombinant BASB019 protein probed with the corresponding anti-recombinant protein sera at 1:200

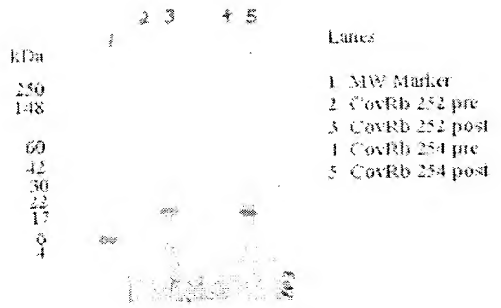

Figure 7: Western-blot of whole cell lysates of 16 strains of *M. Catarrhalis* using pooled sera against the recombinant BASB019 protein. Sera was diluted 1:2000

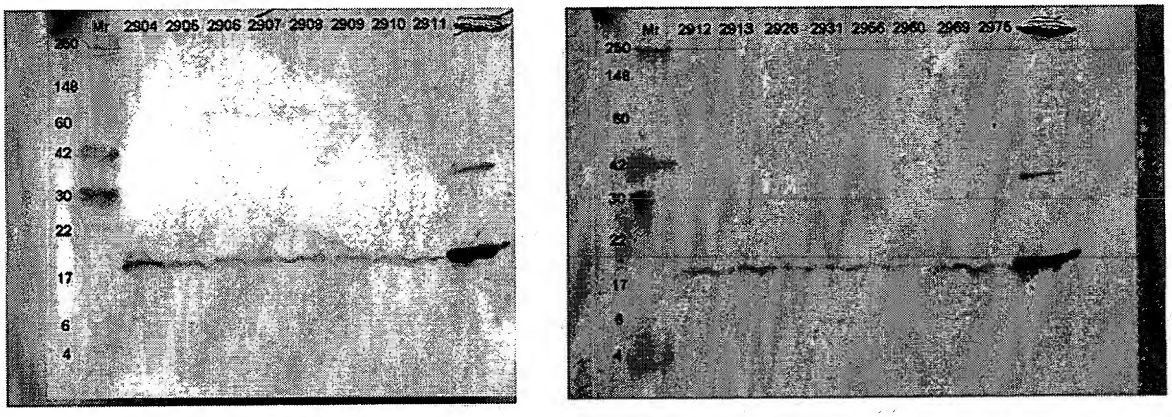

Figure 8: Western-blot of purified recombinant BSAB019 protein probed with pooled human convalescent sera at 1:100